SEQUENCE LISTING

<110> Sahni, Girish
Kumar, Rajesh
Roy, Chaiti
Rajagopal, Kammara
Nihalani, Deepak
Sundaram, Vasudha
Yadav, Mahavir

<120> NOVEL CLOT-SPECIFIC STREPTOKINASE PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID PROTEINS

<130> 07064/009001

<140> US 09/471,349
<141> 1999-12-23

<150> IN 3825/DEL/98
<151> 1998-12-24

<160> 24

<170> FastSEQ for Windows Version 4.0

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<212> DNA
<213> Streptococcus equisimilis

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<221> CDS
<222> (1)...(1242)

<400> 1

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Ile Ala Gly Pro Glu Trp Leu Leu Asp Arg Pro Ser Val Asn Asn Ser
  1               5                  10                  15

caa tta gtt gtt agc gtt gct ggt act gtt gag ggg acg aat caa gac       96
Gln Leu Val Val Ser Val Ala Gly Thr Val Glu Gly Thr Asn Gln Asp
             20                  25                  30

att agt ctt aaa ttt ttt gaa atc gat cta aca tca cga cct gct cat      144
Ile Ser Leu Lys Phe Phe Glu Ile Asp Leu Thr Ser Arg Pro Ala His
         35                  40                  45

gga gga aag aca gag caa ggc tta agt cca aaa tca aaa cca ttt gct      192
Gly Gly Lys Thr Glu Gln Gly Leu Ser Pro Lys Ser Lys Pro Phe Ala
     50                  55                  60

act gat agt ggc gcg atg tca cat aaa ctt gag aaa gct gac tta cta      240
Thr Asp Ser Gly Ala Met Ser His Lys Leu Glu Lys Ala Asp Leu Leu
 65                  70                  75                  80

aag gct att caa gaa caa ttg atc gct aac gtc cac agt aac gac gac      288
Lys Ala Ile Gln Glu Gln Leu Ile Ala Asn Val His Ser Asn Asp Asp
                 85                  90                  95
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tac ttt gag gtc att gat ttt gca agc gat gca acc att act gat cga      336
Tyr Phe Glu Val Ile Asp Phe Ala Ser Asp Ala Thr Ile Thr Asp Arg
            100                 105                 110

aac ggc aag gtc tac ttt gct gac aaa gat ggt tcg gta acc ttg ccg      384
Asn Gly Lys Val Tyr Phe Ala Asp Lys Asp Gly Ser Val Thr Leu Pro
        115                 120                 125

acc caa cct gtc caa gaa ttt ttg cta agc gga cat gtg cgc gtt aga      432
Thr Gln Pro Val Gln Glu Phe Leu Leu Ser Gly His Val Arg Val Arg
    130                 135                 140

cca tat aaa gaa aaa cca ata caa aac caa gcg aaa tct gtt gat gtg      480
Pro Tyr Lys Glu Lys Pro Ile Gln Asn Gln Ala Lys Ser Val Asp Val
145                 150                 155                 160

gaa tat act gta cag ttt act ccc tta aac cct gat gac gat ttc aga      528
Glu Tyr Thr Val Gln Phe Thr Pro Leu Asn Pro Asp Asp Asp Phe Arg
                165                 170                 175

cca ggt ctc aaa gat act aag cta ttg aaa aca cta gct atc ggt gac      576
Pro Gly Leu Lys Asp Thr Lys Leu Leu Lys Thr Leu Ala Ile Gly Asp
            180                 185                 190

acc atc aca tct caa gaa tta cta gct caa gca caa agc att tta aac      624
Thr Ile Thr Ser Gln Glu Leu Leu Ala Gln Ala Gln Ser Ile Leu Asn
        195                 200                 205

aaa aac cac cca ggc tat acg att tat gaa cgt gac tcc tca atc gtc      672
Lys Asn His Pro Gly Tyr Thr Ile Tyr Glu Arg Asp Ser Ser Ile Val
    210                 215                 220

act cat gac aat gac att ttc cgt acg att tta cca atg gat caa gag      720
Thr His Asp Asn Asp Ile Phe Arg Thr Ile Leu Pro Met Asp Gln Glu
225                 230                 235                 240

ttt act tac cgt gtt aaa aat cgg gaa caa gct tat agg atc aat aaa      768
Phe Thr Tyr Arg Val Lys Asn Arg Glu Gln Ala Tyr Arg Ile Asn Lys
                245                 250                 255

aaa tct ggt ctg aat gaa gaa ata aac aac act gac ctg atc tct gag      816
Lys Ser Gly Leu Asn Glu Glu Ile Asn Asn Thr Asp Leu Ile Ser Glu
            260                 265                 270

aaa tat tac gtc ctt aaa aaa ggg gaa aag ccg tat gat ccc ttt gat      864
Lys Tyr Tyr Val Leu Lys Lys Gly Glu Lys Pro Tyr Asp Pro Phe Asp
        275                 280                 285

cgc agt cac ttg aaa ctg ttc acc atc aaa tac gtt gat gtc gat acc      912
Arg Ser His Leu Lys Leu Phe Thr Ile Lys Tyr Val Asp Val Asp Thr
    290                 295                 300

aac gaa ttg cta aaa agt gag cag ctc tta aca gct agc gaa cgt aac      960
Asn Glu Leu Leu Lys Ser Glu Gln Leu Leu Thr Ala Ser Glu Arg Asn
305                 310                 315                 320

tta gac ttc aga gat tta tac gat cct cgt gat aag gct aaa cta ctc     1008
Leu Asp Phe Arg Asp Leu Tyr Asp Pro Arg Asp Lys Ala Lys Leu Leu
                325                 330                 335
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tac aac aat ctc gat gct ttt ggt att atg gac tat acc tta act gga      1056
Tyr Asn Asn Leu Asp Ala Phe Gly Ile Met Asp Tyr Thr Leu Thr Gly
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aaa gta gag gat aat cac gat gac acc aac cgt atc ata acc gtt tat      1104
Lys Val Glu Asp Asn His Asp Asp Thr Asn Arg Ile Ile Thr Val Tyr
        355                 360                 365

atg ggc aag cga ccc gaa gga gag aat gct agc tat cat tta gcc tat      1152
Met Gly Lys Arg Pro Glu Gly Glu Asn Ala Ser Tyr His Leu Ala Tyr
    370                 375                 380

gat aaa gat cgt tat acc gaa gaa gaa cga gaa gtt tac agc tac ctg      1200
Asp Lys Asp Arg Tyr Thr Glu Glu Glu Arg Glu Val Tyr Ser Tyr Leu
385                 390                 395                 400

cgt tat aca ggg aca cct ata cct gat aac cct aac gac aaa              1242
Arg Tyr Thr Gly Thr Pro Ile Pro Asp Asn Pro Asn Asp Lys
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<210> 2
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<213> Streptococcus equisimilis

<400> 2

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            20                  25                  30
Ile Ser Leu Lys Phe Phe Glu Ile Asp Leu Thr Ser Arg Pro Ala His
        35                  40                  45
Gly Gly Lys Thr Glu Gln Gly Leu Ser Pro Lys Ser Lys Pro Phe Ala
    50                  55                  60
Thr Asp Ser Gly Ala Met Ser His Lys Leu Glu Lys Ala Asp Leu Leu
65                  70                  75                  80
Lys Ala Ile Gln Glu Gln Leu Ile Ala Asn Val His Ser Asn Asp Asp
                85                  90                  95
Tyr Phe Glu Val Ile Asp Phe Ala Ser Asp Ala Thr Ile Thr Asp Arg
            100                 105                 110
Asn Gly Lys Val Tyr Phe Ala Asp Lys Asp Gly Ser Val Thr Leu Pro
        115                 120                 125
Thr Gln Pro Val Gln Glu Phe Leu Leu Ser Gly His Val Arg Val Arg
    130                 135                 140
Pro Tyr Lys Glu Lys Pro Ile Gln Asn Gln Ala Lys Ser Val Asp Val
145                 150                 155                 160
Glu Tyr Thr Val Gln Phe Thr Pro Leu Asn Pro Asp Asp Asp Phe Arg
                165                 170                 175
Pro Gly Leu Lys Asp Thr Lys Leu Leu Lys Thr Leu Ala Ile Gly Asp
            180                 185                 190
Thr Ile Thr Ser Gln Glu Leu Leu Ala Gln Ala Gln Ser Ile Leu Asn
        195                 200                 205
Lys Asn His Pro Gly Tyr Thr Ile Tyr Glu Arg Asp Ser Ser Ile Val
    210                 215                 220
Thr His Asp Asn Asp Ile Phe Arg Thr Ile Leu Pro Met Asp Gln Glu
225                 230                 235                 240
Phe Thr Tyr Arg Val Lys Asn Arg Glu Gln Ala Tyr Arg Ile Asn Lys
                245                 250                 255
Lys Ser Gly Leu Asn Glu Glu Ile Asn Asn Thr Asp Leu Ile Ser Glu
            260                 265                 270
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Lys Tyr Tyr Val Leu Lys Lys Gly Glu Lys Pro Tyr Asp Pro Phe Asp
        275                 280                 285
Arg Ser His Leu Lys Leu Phe Thr Ile Lys Tyr Val Asp Val Asp Thr
    290                 295                 300
Asn Glu Leu Leu Lys Ser Glu Gln Leu Leu Thr Ala Ser Glu Arg Asn
305                 310                 315                 320
Leu Asp Phe Arg Asp Leu Tyr Asp Pro Arg Asp Lys Ala Lys Leu Leu
                325                 330                 335
Tyr Asn Asn Leu Asp Ala Phe Gly Ile Met Asp Tyr Thr Leu Thr Gly
            340                 345                 350
Lys Val Glu Asp Asn His Asp Asp Thr Asn Arg Ile Ile Thr Val Tyr
        355                 360                 365
Met Gly Lys Arg Pro Glu Gly Glu Asn Ala Ser Tyr His Leu Ala Tyr
    370                 375                 380
Asp Lys Asp Arg Tyr Thr Glu Glu Glu Arg Glu Val Tyr Ser Tyr Leu
385                 390                 395                 400
Arg Tyr Thr Gly Thr Pro Ile Pro Asp Asn Pro Asn Asp Lys
                405                 410
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<210> 3
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(777)

<400> 3

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Gln Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln
  1               5                  10                  15

agc aag ccc ggt tgt tat gac aat gga aaa cac tat cag ata aat caa       96
Ser Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln
            20                  25                  30

cag tgg gag cgg acc tac cta ggt aat gtg ttg gtt tgt act tgt tat      144
Gln Trp Glu Arg Thr Tyr Leu Gly Asn Val Leu Val Cys Thr Cys Tyr
        35                  40                  45

gga gga agc cga ggt ttt aac tgc gaa agt aaa cct gaa gct gaa gag      192
Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu
    50                  55                  60

act tgc ttt gac aag tac act ggg aac act tac cga gtg ggt gac act      240
Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr
65                  70                  75                  80

tat gag cgt cct aaa gac tcc atg atc tgg gac tgt acc tgc atc ggg      288
Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly
                85                  90                  95

gct ggg cga ggg aga ata agc tgt acc atc gca aac cgc tgc cat gaa      336
Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu
            100                 105                 110

ggg ggt cag tcc tac aag att ggt gac acc tgg agg aga cca cat gag      384
Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu
        115                 120                 125
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```
act ggt ggt tac atg tta gag tgt gtg tgt ctt ggt aat gga aaa gga      432
Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly
    130                 135                 140

gaa tgg acc tgc aag ccc ata gct gag aag tgt ttt gat cat gct gct      480
Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala
145                 150                 155                 160

ggg act tcc tat gtg gtc gga gaa acg tgg gag aag ccc tac caa ggc      528
Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly
                165                 170                 175

tgg atg atg gta gat tgt act tgc ctg gga gaa ggc agc gga cgc atc      576
Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile
            180                 185                 190

act tgc act tct aga aat aga tgc aac gat cag gac aca agg aca tcc      624
Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser
        195                 200                 205

tat aga att gga gac acc tgg agc aag aag gat aat cga gga aac ctg      672
Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu
    210                 215                 220

ctc cag tgc atc tgc aca ggc aac ggc cga gga gag tgg aag tgt gag      720
Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu
225                 230                 235                 240

agg cac acc tct gtg cag acc aca tcg agc gga tct ggc ccc ttc acc      768
Arg His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr
                245                 250                 255

gat gtt cgt                                                         777
Asp Val Arg
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<210> 4
<211> 259
<212> PRT
<213> Homo sapiens

<400> 4

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Gln Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln
  1               5                  10                  15
Ser Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln
            20                  25                  30
Gln Trp Glu Arg Thr Tyr Leu Gly Asn Val Leu Val Cys Thr Cys Tyr
        35                  40                  45
Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu
    50                  55                  60
Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr
65                  70                  75                  80
Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly
                85                  90                  95
Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu
            100                 105                 110
Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu
        115                 120                 125
Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly
    130                 135                 140
```

```
Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala
145                 150                 155                 160
Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly
                165                 170                 175
Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile
            180                 185                 190
Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser
        195                 200                 205
Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu
    210                 215                 220
Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu
225                 230                 235                 240
Arg His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr
                245                 250                 255
Asp Val Arg
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<210> 5
<211> 1377
<212> DNA
<213> Streptococcus equisimilis

<400> 5

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agatatacca tgattgctgg acctgagtgg ctgctagacc gtccatctgt caacaacagc     180
caattggttg ttagcgttgc tggtactgtt gaggggacga atcaagacat tagtcttaaa     240
ttttttgaaa tcgatctaac atcacgacct gctcatggag gaaagacaga gcaaggctta     300
agtccaaaat caaaaccatt tgctactgat agtggcgcga tgtcacataa acttgagaaa     360
gctgacttac taaaggctat tcaagaacaa ttgatcgcta acgtccacag taacgacgac     420
tactttgagg tcattgattt tgcaagcgat gcaaccatta ctgatcgaaa cggcaaggtc     480
tactttgctg acaaagatgg ttcggtaacc ttgccgaccc aacctgtcca agaatttttg     540
ctaagcggac atgtgcgcgt tagaccatat aaagaaaaac caatacaaaa ccaagcgaaa     600
tctgttgatg tggaatatac tgtacagttt actcccttaa accctgatga cgatttcaga     660
ccaggtctca aagatactaa gctattgaaa acactagcta tcggtgacac catcacatct     720
caagaattac tagctcaagc acaaagcatt ttaaacaaaa accacccagg ctatacgatt     780
tatgaacgtg actcctcaat cgtcactcat gacaatgaca ttttccgtac gattttacca     840
atggatcaag agtttactta ccgtgttaaa aatcgggaac aagcttatag gatcaataaa     900
aaatctggtc tgaatgaaga aataaacaac actgacctga tctctgagaa atattacgtc     960
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aatgctagct atcatttagc ctatgataaa gatcgttata ccgaagaaga acgagaagtt    1320
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<212> DNA
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<220>
<223> Synthetically generated primer

<400> 6

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aaataacagc caattggttg ttagcgttgc tggtactgtt gaggggacga atcaagacat     180
tagtcttaaa ttttttgaaa tcgatctaac atcacgacct gctcatggag gaaagacaga     240
gcaaggctta agtccaaaat caaaaccatt tgctactgat agtggcgcga tgtcacataa     300
acttgagaaa gctgacttac taaaggctat tcaagaacaa ttgatcgcta acgtccacag     360
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

<221> CDS
<222> (2)...(52)

<400> 7
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1 5 10 15

ccc 52
Pro

<210> 8
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated protein

<400> 8
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1 5 10 15
Pro

<210> 9
<211> 1541
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

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atcaagacat tagtcttaaa ttttttgaaa tcgatctaac atcacgacct gctcatggag 180
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<210> 10
<211> 1661
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

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taaaggctat tcaagaacaa ttgatcgcta acgtccacag taacgacgac tactttgagg 480
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agtttactta ccgtgttaaa aatcgggaac aagcttatag gatcaataaa aaatctggtc 960
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gggagcggac ctacctaggt aatgtgttgg tttgtacttg ttatggagga agccgaggtt 1500

ttaactgcga aagtaaacct gaagctgaag agacttgctt tgacaagtac actgggaaca 1560
cttaccgagt gggtgacact tatgagcgtc ctaaagactc catgatctgg gactgtacct 1620
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<211> 1782
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<220>
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<220>
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<211> 53
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<220>
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<210> 14
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<400> 14
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<210> 15
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<400> 15
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<210> 16
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<212> DNA
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<400> 16
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<210> 22
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<210> 23
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<400> 23
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<210> 24
<211> 27
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<400> 24
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